WHAT IS CLAIMED:

1.   A method of identifying cancer specific marker genes, comprising:

preparing clones by transforming DNA of interest into plasmids, said plasmids each containing a single clone;

providing a tissue array containing multiple cancer tissue samples;

providing a pool of said clones and hybridizing said clones with said cancer tissue samples on said tissue array; and

screening and identifying clones displaying positive hybridization with said cancer tissue samples.

2.   The method of claim 1, wherein said cancer is lung cancer.

3.   The method of claim 1, wherein said multiple cancer tissue samples each contains a different type of cancer tissue.

4.   The method of claim 2, wherein said clones displaying positive hybridization with said cancer tissue samples have any of the polynucleotide sequences provided in SEQ Nos. 1-7.

5.   The method of claim 1, further comprising identifying one or more clinical phenotypes expressed by each of said clones.

6.   The method of claim 5, wherein said phenotypes include cancer histotypes, developmental stages, responsiveness to various therapies, and survival/death rates.

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7.   A method of identifying genes overexpressed in lung cancer tissues, comprising:

preparing candidate lung cancer specific clones by transforming DNA of interest;

providing tissue samples of lung cancer;

providing a pool of said clones and hybridizing said clones with said tissue

5   samples; and

determining whether said pool of said clones positively hybridizes with said

cancer tissue samples; and

screening and identifying each individual clone responsible for positive

hybridization.

10   8.   The method of claim 7, wherein said clone has any of the polynucleotide

sequences provided in SEQ Nos. 1-7.

9.   The method of claim 7, further comprising identifying clinical phenotypes

expressed by said clone.

10.   The method of claim 9, wherein said phenotypes include cancer histotypes,

15   developmental stages, responsiveness to various therapies, and survival/death

rates.

11.   A method of detecting a cancer in a patient, comprising:

contacting a biological sample obtained from a patient with an oligonucleotide

that hybridizes to a polynucleotide that is identified as lung tumor specific;

20   detecting in the sample a level of a polynucleotide that hybridizes to the

oligonucleotide; and

comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

12. The method of claim 11, wherein said cancer is lung cancer.

13. The method of claim 11, wherein said polynucleotide that is identified as lung tumor specific is identified according to the method of claim 1 or claim 7.

14. A method of monitoring the progression of a cancer in a patient, comprising:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide identified as lung cancer specific;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

15. The method of claim 14, wherein said cancer is lung cancer.

16. The method of claim 14, wherein said polynucleotide that is identified as lung tumor specific is identified according to the method of claim 1 or claim 7.